

# Genome Sequence of the Mucoromycotina Fungus *Umbelopsis isabellina*, an Effective Producer of Lipids

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***Umbelopsis isabellina* is a fungus in the subdivision Mucoromycotina, many members of which have been shown to be oleaginous and have become important organisms for producing oil because of their high level of intracellular lipid accumulation from various feedstocks. The genome sequence of *U. isabellina* NBRC 7884 was determined and annotated, and this information might provide insights into the oleaginous properties of this fungus.**

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*Umbelopsis isabellina* is a Mucoromycotina fungus belonging to the order Mucorales, which includes the genera *Rhizopus*, *Mucor*, *Cunninghamella*, etc. Interestingly, *U. isabellina* was formerly classified in the order Mortierellales, but a molecular phylogenetic analysis has shown that *Umbelopsis* species belong in the Mucorales order (1).

Many fungi in the subdivision Mucoromycotina, including the well-known pathogen *Rhizopus oryzae*, have been shown to be oleaginous (2, 3). Both *U. isabellina* and *Cunninghamella echinulata* accumulate lipids to more than 40% of their biomass (4). Because of their high levels of intracellular triacylglyceride accumulation, versatility in nutrient utilization, and high growth rate, Mucoromycotina fungi are becoming increasingly important as potential producers of biofuels and high-value chemicals (5, 6). The genome sequences of at least two Mucoromycotina fungi have been published—*R. oryzae* (7) and the Mortierellales fungus *Mortierella alpina* (3). Moreover, other genome sequences are currently accessible through the Joint Genome Institute (JGI) Mycocosm Genome Portal (8), including *Mucor circinelloides*, *Umbelopsis rammanniana*, and *Phycomyces blakesleeana*. However, the numbers of Mucoromycotina genome sequences are still much lower than those of other lineages of Dikarya fungi. The comparative study of the Mucoromycotina fungi could be useful for determining the genetic factors related to oleaginous characteristics because they share oleaginous characteristics. However, only small regions of microsynteny have been observed among the genome sequences currently available (our unpublished data).

The fungal strain used in this study, *U. isabellina* NBRC 7884, was obtained from the Japanese Biological Resource Center, NITE (<http://www.nbrc.nite.go.jp/>). Whole-genome sequencing was performed using a mate-paired library with an insert size of approximately 3 kb and a read length of 55 bases with the SOLiD 5500xl system (Life Technologies). The total short reads were fil-

tered according to quality (9), resulting in approximately 200-fold coverage (85,662,706 reads), and assembled by SOLiD De Novo Accessory Tools 2.0 (Life Technologies), which contains the Velvet assembler (10), with a k-mer size of 37. The assembly generated 84 scaffolds ( $\geq 1$  kb) with an  $N_{50}$  value of 554,975 bp and a maximum length of 1,873,367 bp. The assembled genome of 22,588,838 bp was covered by 84 scaffolds, including 53 scaffolds of  $>100$  kb and 4 scaffolds of  $>1$  Mb, with a G+C content of 41.79%.

A total of 9,081 protein-coding genes were predicted, based on the homologies to known genes and the statistical features of the genes, by applying a combination of gene-finding software tools (11). Functional annotation of the genes was predicted by a homology search (BLASTp) against an NCBI-nr protein database. A total of 6,911 of 9,081 protein-coding genes (76.1%) were homologous to sequences in the annotated genes of *U. rammanniana* sequenced by the Department of Energy (DOE) Joint Genome Institute (8) (BLASTp  $E$  value,  $1e-5$ ; sequence length,  $\leq 20\%$  difference; and sequence identity,  $\geq 25\%$ ).

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession numbers [BAVE01000001](https://www.ncbi.nlm.nih.gov/nuclseq/BAVE01000001) through [BAVE01000084](https://www.ncbi.nlm.nih.gov/nuclseq/BAVE01000084). The version described in this paper is the first version.

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